

JD Vogt

Portfolio selections of recent work - (but doesn't yet include Salesforce)

This document contains examples and descriptions of recent work as a ux/product designer. Additional examples of my work can be found at www.jdvogt.com.

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Snapzing

Snapzing is a social photo game app I co-created for the iPhone. The app was designed and developed by myself and my co-founder.

How it works

Users are given a photography goal with an allotted time to enter pictures. Users then rate photos through a "face-off" interface. (It's fun!). The winner receives a real prize.

Contribution

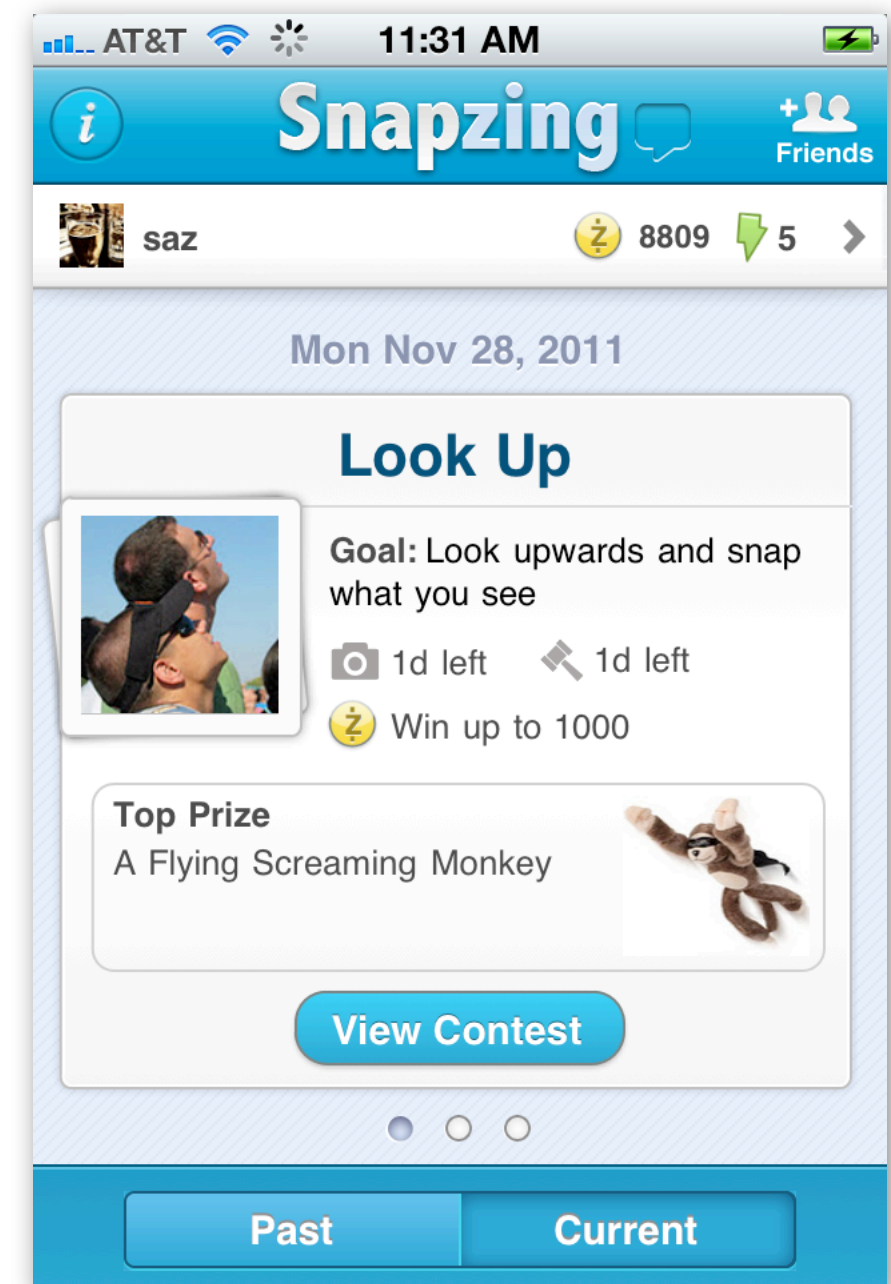
Concept, wireframing, visual design, assets, interaction design, usability testing. Just about everything but code.

Design challenges

There were a number of design challenges to work through such as welcoming newcomers, encouraging contribution, creating a crowd-source rating system and clearly conveying picture "state" to the user.

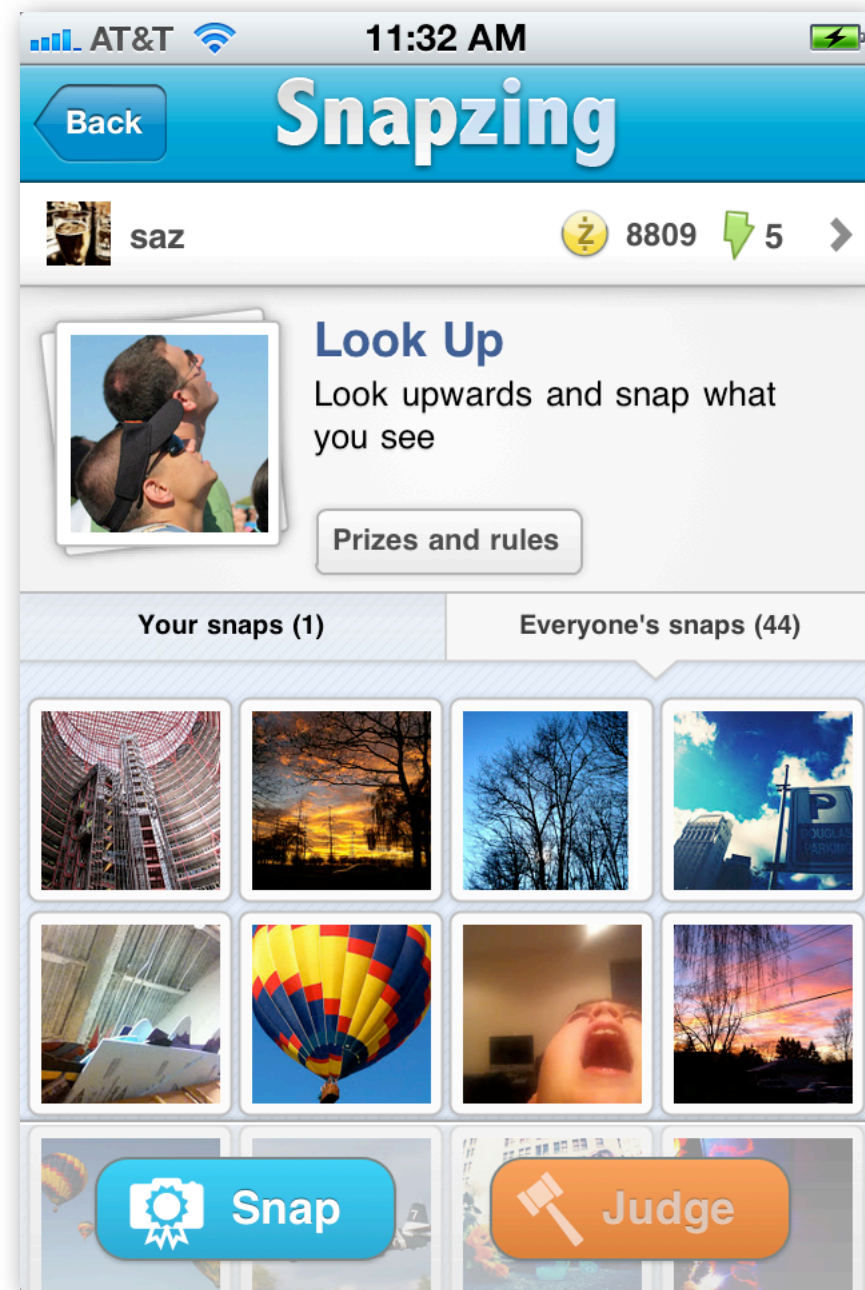


Past contest screen

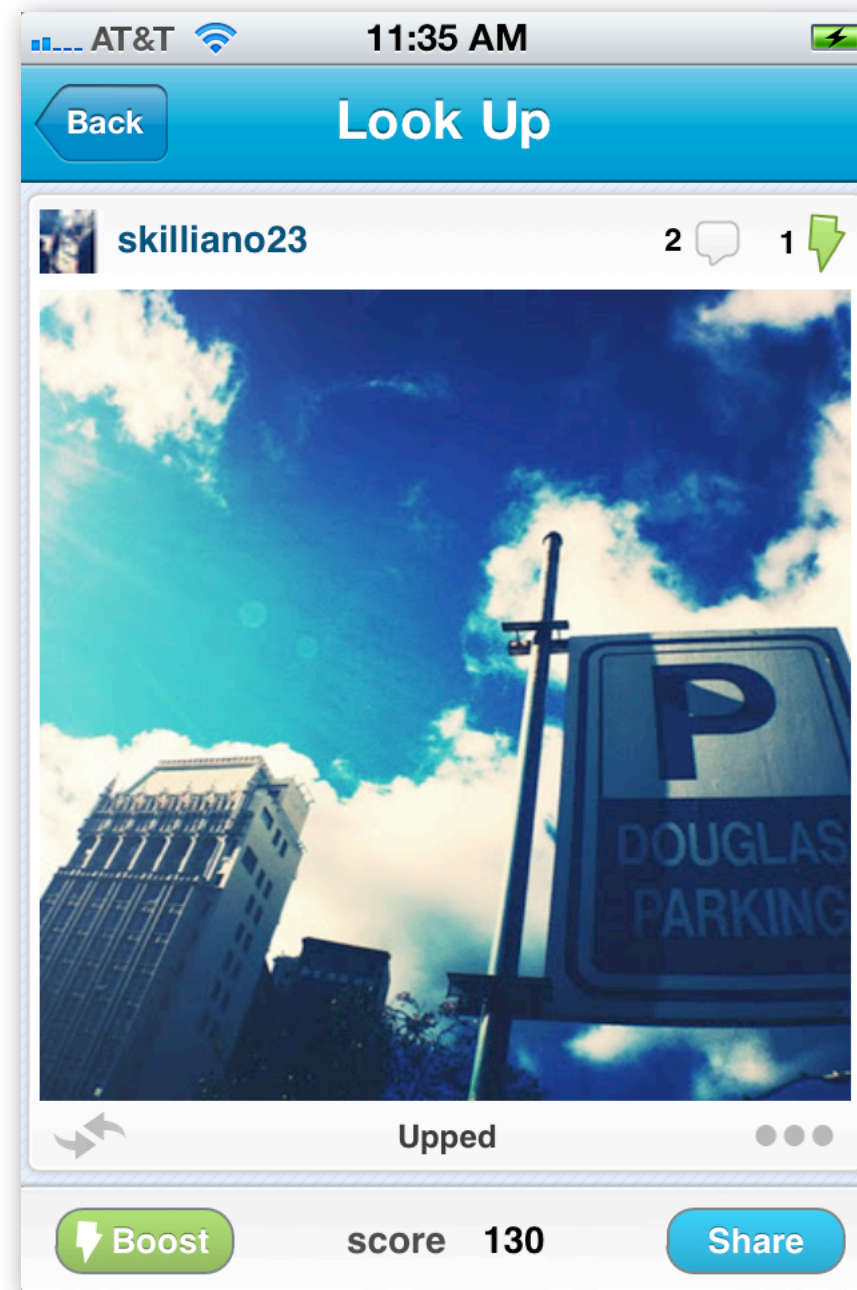


Current contests to enter

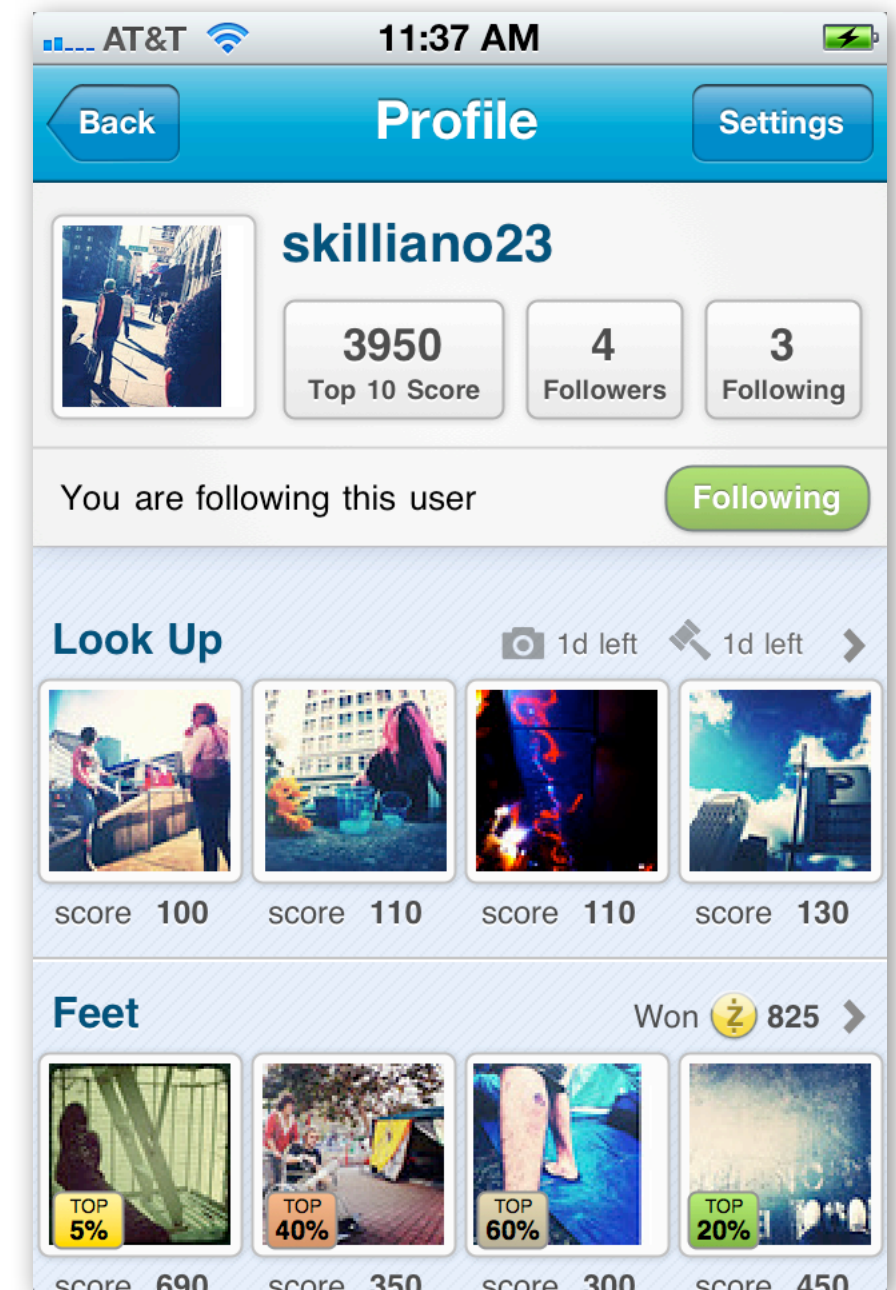
Snapzing



Contest detail screen - A tab separates a user's photos from everyone else's. Large clear buttons clue the user in on the most important actions.

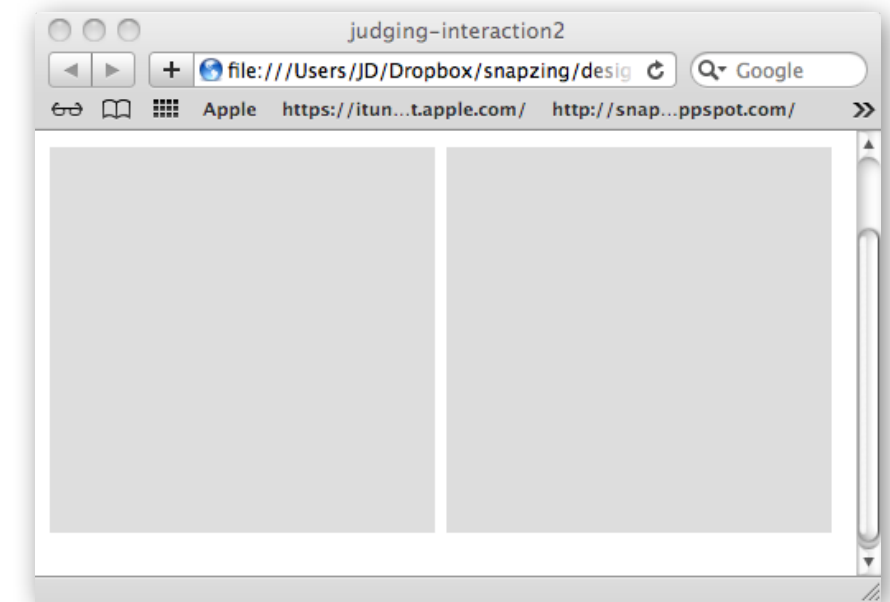
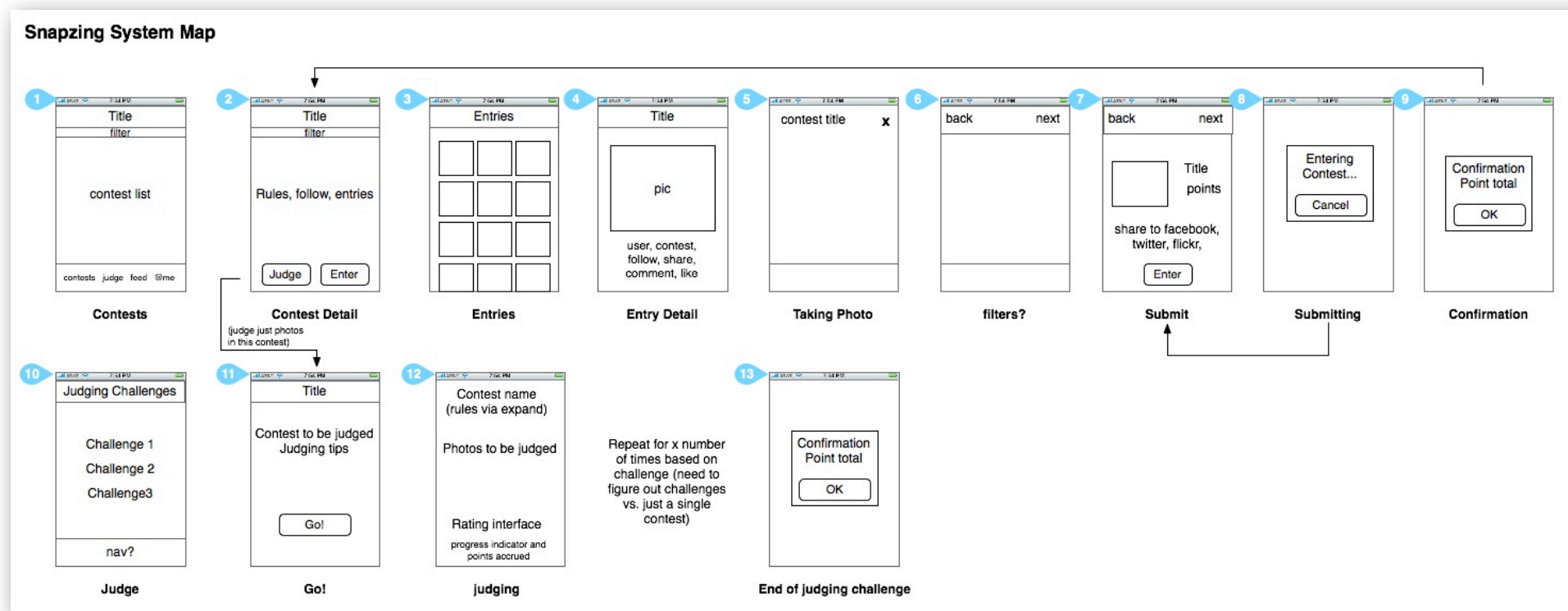


Picture detail screen - By assigning stats to a photo like number of comments, score, and boosts, users gain recognition and a sense of validation for their submissions. This encourages future contributions.

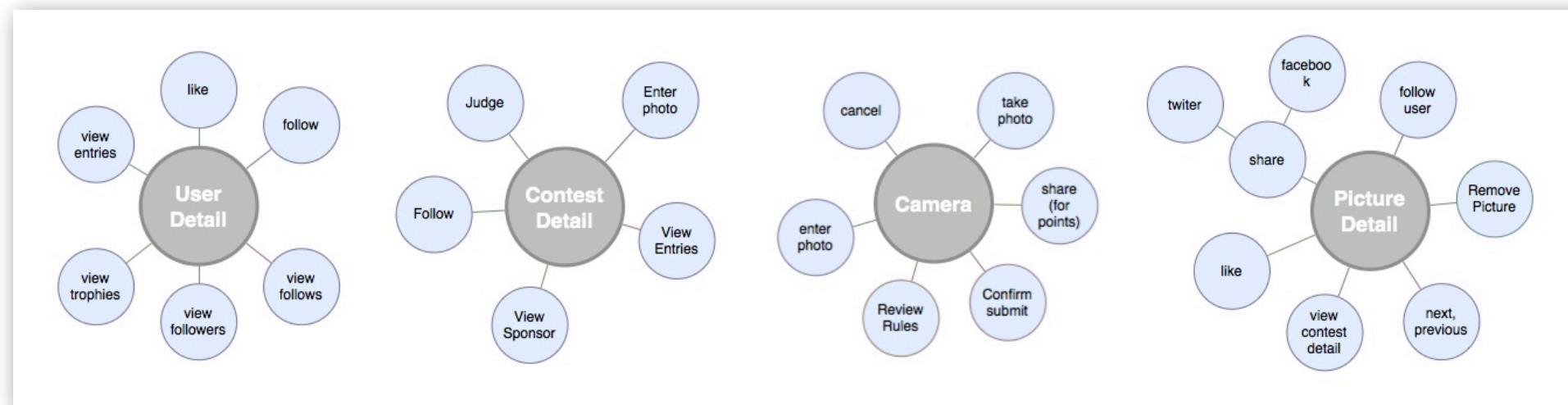


User profile page - Users can follow, have followers, and see how their photos have done in past contests. These and other social mechanisms help establish a sense of community.

Snapzing



I created a Flash prototype of the judging interaction to test how side by side judging would feel.



An early system map above and hub and spoke diagram beneath. I used the system map to explore how the app should flow and how a user would move from screen to screen.



The final judging interaction. - Pictures are awarded 10 points each time one is chosen over the other.

blueGuru for jetBlue

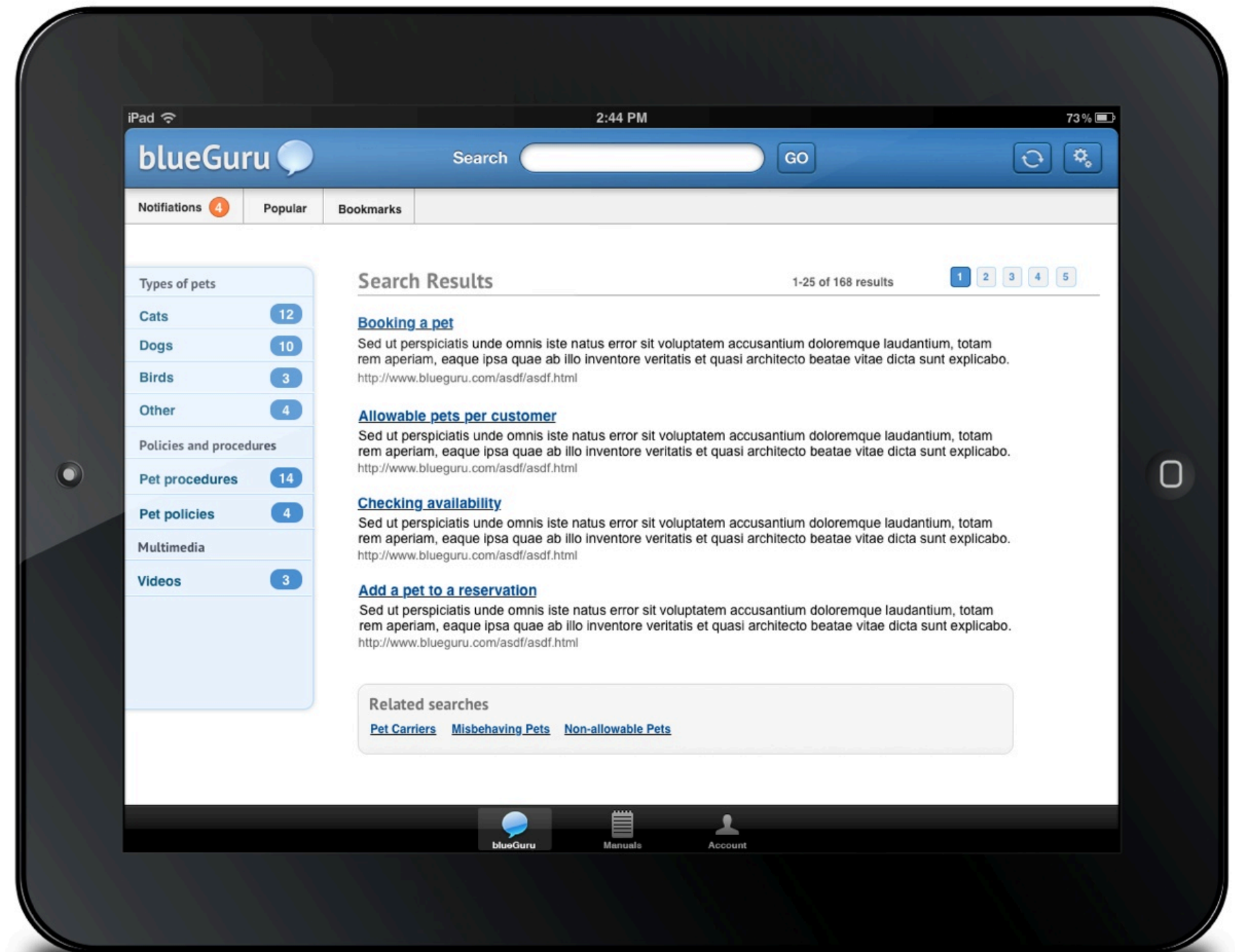
You might have seen news reports of airlines testing out iPads in the cockpit. This project for jetBlue is such a product, and is designed for use by other airline personnel as well.

blueGuru is envisioned as an html5 answer engine to run on various devices and work not just in the cockpit, but also on the ground, ramp, or in an office, taking the place of expensive printed manuals.

Contribution

- Facilitating product ideation
- Wireframing & product design
- Information architecture and search design

This product has not yet been released

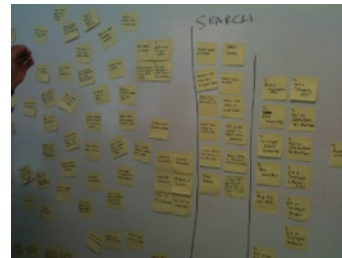
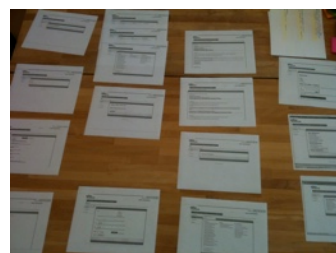


A mockup of jetBlue's blueGuru on a tablet

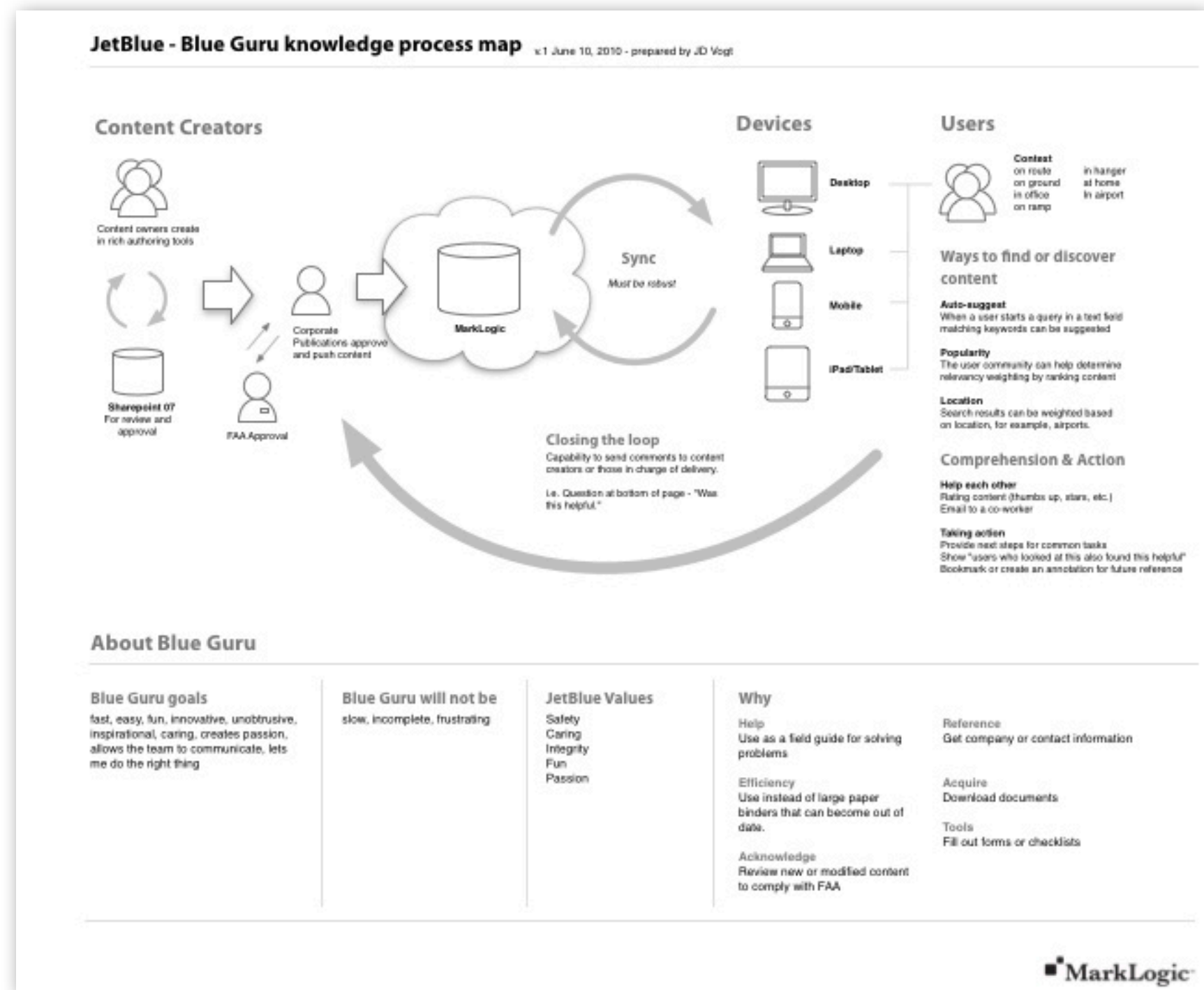
The MarkLogic field staff had already created a web app but there were some issues with the implementation such as poor information scent and an unintuitive flow.

Kickoff

By facilitating a reboot kickoff meeting, I had the chance to meet with both the content providers and the content consumers. I performed a KJ exercise to determine the information hierarchy and discover the tasks that users found most important. We included stakeholders and users from 7 different departments in these meetings.



Snapshots from the kickoff meetings.



Knowing how information flows in and out of the app is key to its improvement and longevity. I created this diagram to help the publications team and myself understand how the app would work as part of a larger ecosystem of users, devices, and content evolution.

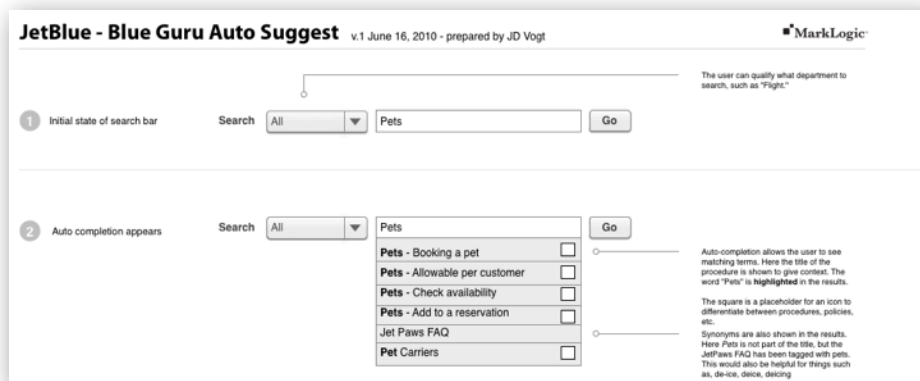
Humanizing content

As we examined the existing content, it became clear that it was written with regulations in mind.

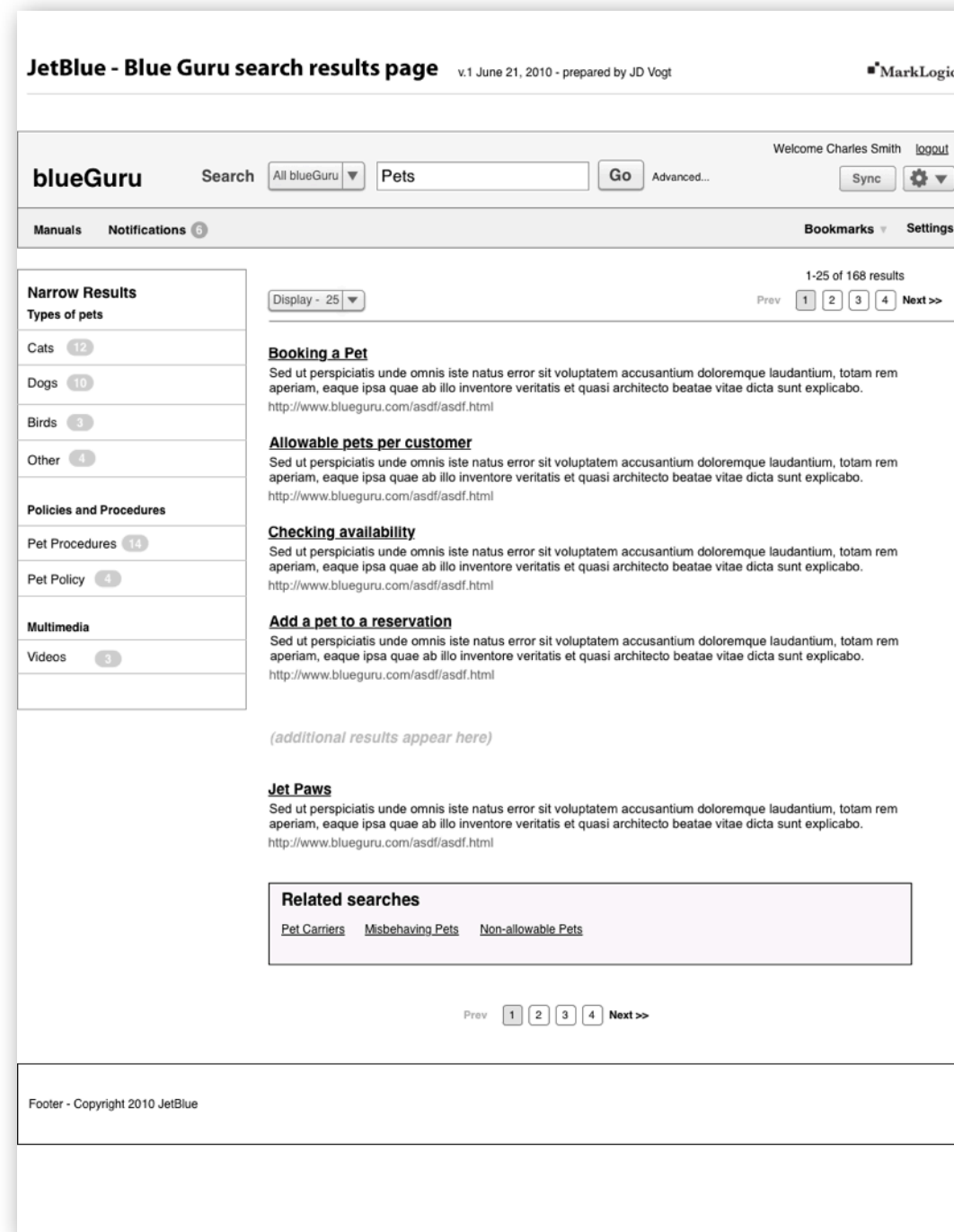
Interviews with end users revealed that they didn't much care for the hierarchies, they just wanted an answer to their problem. Re-writing the topics and headlines was crucial for users to easily scan and hone in on important content. Content is still king.

Search and social

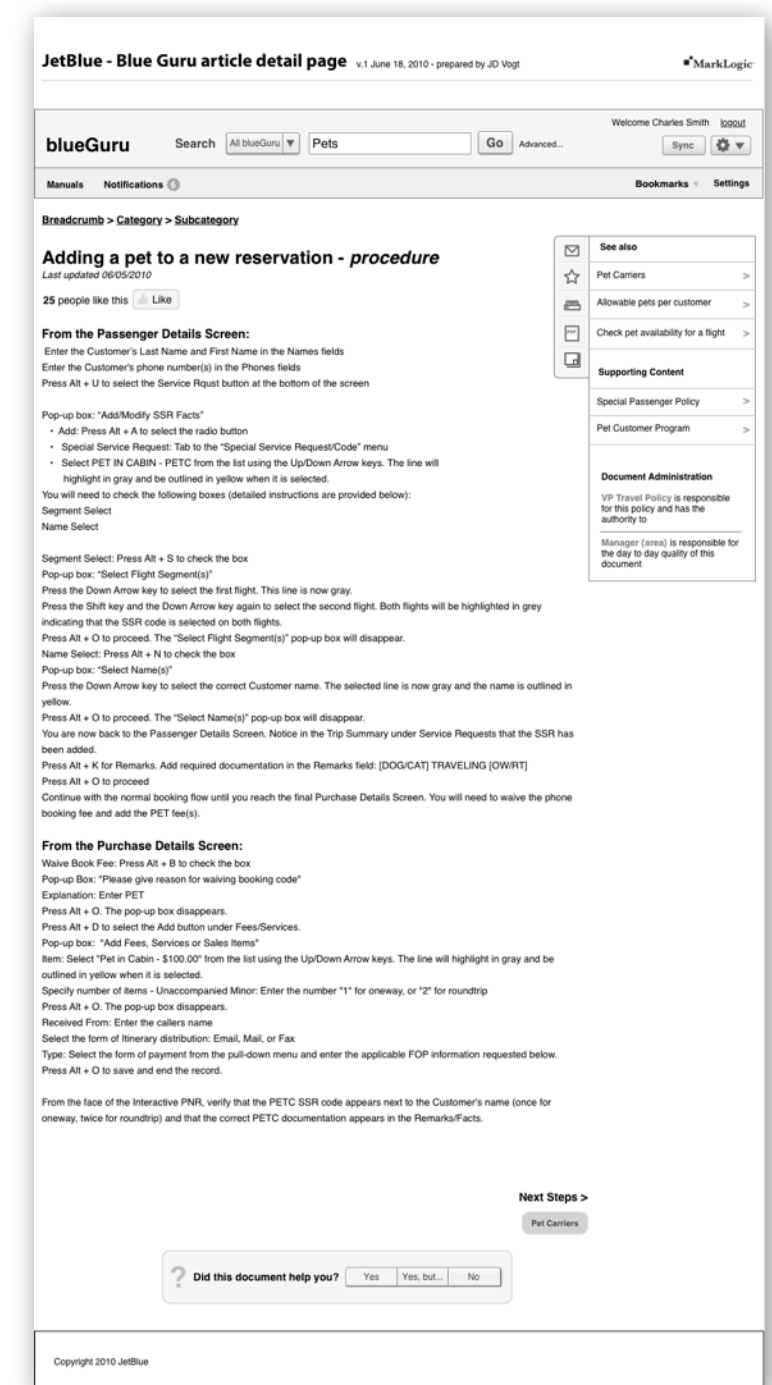
We also incorporated search and social patterns into the new design, such as auto suggest, facets, pagination, better information scent, and a feedback/rating system.



A wireframe demonstrating the interactions for the type-ahead search interface.



A wireframe showing a search result for policies on pets. How many pets can you bring on board? Three, it turns out.



A wireframe of a topic detail. Users are encouraged to rate or give feedback on the content.

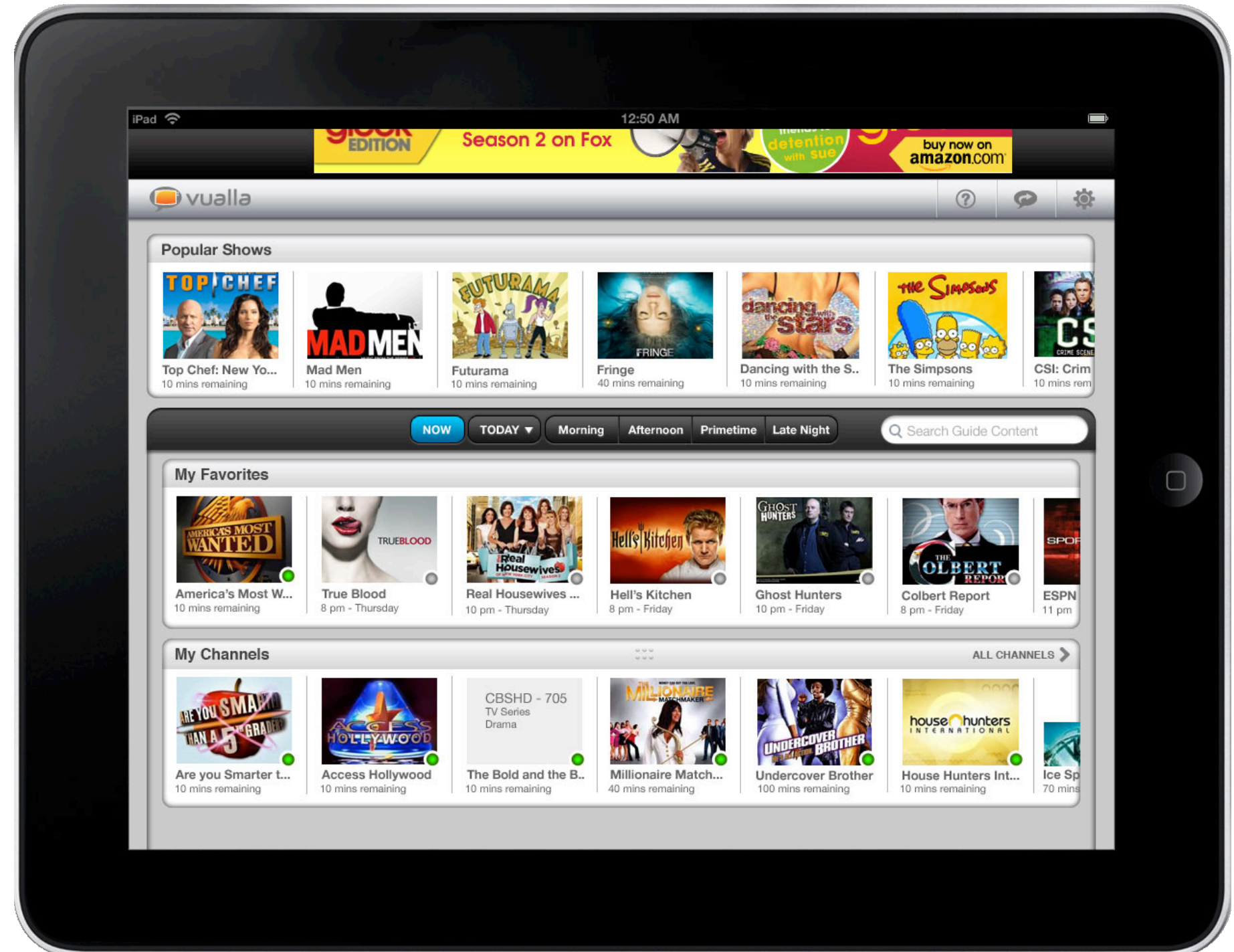
Vualla

Vualla was originally conceived as an iPad remote control. Through the ideation activities I conducted with the team, it morphed into a platform for social television - letting users know what others were watching and tweeting about.

While innovative at the time, other apps have moved into this space and Vualla is no longer in development. My work on this app was as an independent contractor.

Contribution

- Facilitating product ideation
- Product research
- Storyboarding
- Wireframing
- Heuristic evaluation of designs
- Usability testing



The Vualla main interface screen for selecting shows

Vualla



Snapshots of clients participating in an ideation meeting where I led a storyboard “speed-dating” and KJ session. The methodology guided us in reframing the app from being merely a remote to becoming a guide to finding content based on one’s social graph.

Vualla Usability Test			Date	Version
Participant name	Size of TV	iPad or similar device		
Gender	Smart phone	Laptop		
Occupation	Game System	Desktop		
Hours TV watched/week	iPod or similar device			
Application Launch You've heard about a new app on the appstore called Vualla, that had some good reviews and you decided to download it and check it out.				
Splash reaction NOTES				
Choose provider NOTES		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Choose favorites NOTES		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Show or hide a category from the listing NOTES		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

I created and conducted usability tests on a prototype product in a mock living room. Because this was a casual product and there was an inherent sense of flow, I asked users to play with the app as if they had just downloaded it. As users worked through the app, I marked down the ease or difficulty they had in discovering features and accomplishing tasks.

While this approach worked well, the end results of usability testing were a mixed bag. Some users breezed through the app, others stumbled early and often.



A content detail screen with Facebook comments and Twitter tweets incorporated into the interface.

HFinder

What is it HFinder? A Social knowledge and machine learning engine for discovering and rating bioinformatics hypotheses. Quite a mouthful, but a very cool concept.

How it works

Scientific papers on pathology and bioinformatics are fed into a semantic database. The system creates hypotheses based on the aggregate information across domains to make scientific predictions. Scientists (the users) rate the hypotheses and debate their relative merit.

Contribution

Product design and research, ecosystem design, search and discovery design, rating design, wireframing.

Design challenge

Turn a database into a social collaboration platform. Additionally, create a rating system that was richer than stars or "likes."

The screenshot displays the HFinder website interface. At the top right, it says "Welcome Ramon Felciano" with a "logout" link. The main header features the "INGENUITY SYSTEMS" logo, a search bar, and a "Go" button. Below the header, there are navigation links for "Home", "Leaderboard", "Hypotheses", and "Watchlist".

The "Leaderboard" section is the primary focus. It includes a filter for "pathogen: Ebola", a "Sort by: Biology Rating" dropdown, and a "Display - 10" dropdown. The results are shown as a list of hypotheses, each with a community rank represented by a grid of colored squares (green for high, yellow for medium, grey for low). The hypotheses listed are:

- Inhibiting RAC1 would counteract Ebola pathogenesis**: 13 score, 11 ratings, 14 findings, 3 comments, 1 pathogen, 78 genes. Status: In vitro: verified, Ex vivo: failed, In vivo: --.
- Inhibiting SERPINE1 would counteract Ebola pathogenesis**: 12 score, 9 ratings, 12 findings, 5 comments, 5 pathogen, 78 genes. Status: In vitro: verified, Ex vivo: failed, In vivo: --.
- Activating INS1 would counteract Ebola pathogenesis**: 9 score, 10 ratings, 12 findings, 5 comments, 5 pathogen, 78 genes. Status: In vitro: verified, Ex vivo: failed, In vivo: --.
- Inhibiting TFGB1 would counteract Ebola pathogenesis**: 8 score, 10 ratings, 14 findings, 2 comments, 1 pathogen, 36 genes. Status: In vitro: verified, Ex vivo: failed, In vivo: --.

On the left side, there is a "My Ratings" section with checkboxes for "very promising (12)", "promising (34)", "neutral (4)", "concerns (23)", and "major concerns (14)", along with an "Unrated (4,756)" option. Below this are sections for "Virus (4657)", "Bacteria (2045)", "Intervention", "Affected Pathogens", and "Disease".

A wireframe of the leaderboard page. Hypotheses can be filtered by the faceted navigation on the left. The results in the center display the community rank and provide detailed scent about the hypothesis via icons and descriptions. I

HFinder

Designing an appropriate rating system

Since users would be rating hypotheses, my first thought was to use stars as the rating system. Users are generally familiar with stars, they don't require a lot of explanation and there are established design patterns. (Netflix for instance) "Done!" I thought.







But scientists would be ranking things more akin to a Likert scale where one agreed or disagreed with the hypothesis.

Stars weren't the right fit because they have one axis that moves from left to right. They're not bi-axial where choices can be negative, neutral or positive.







In the resulting interface, a user chooses between 5 values with the far left being the most negative, and the far right being the most positive. Selecting the middle square is a neutral rating.

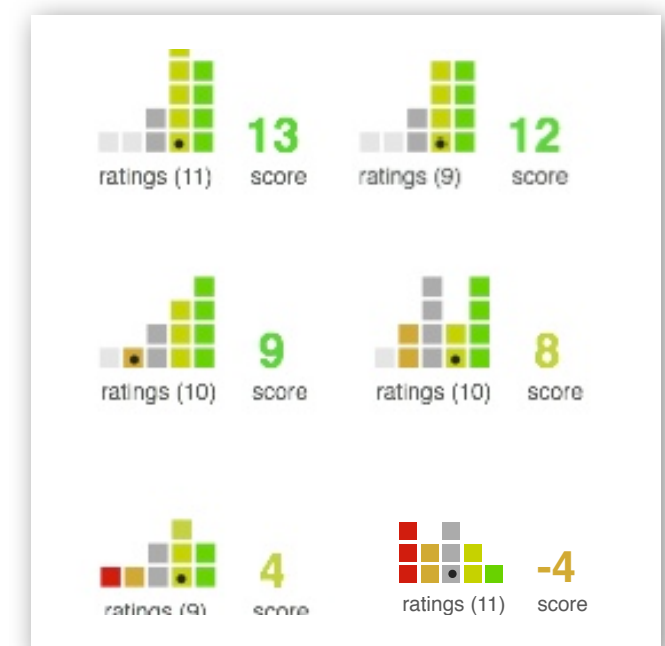
The line in the middle gives a visual indication of the balancing point. Color and position are used to show a user's rating.

Scoring an unranked item interaction

-  1 An unranked hypothesis is shown as empty
-  2 As the user hovers over a square, the value for that square appears to the right
-  3 Hovering over a different square shows its color and value
-  4 Clicking a square saves the score, square outline changes from gray to black.
-  5 The save badge brightens when save is complete
-  6 The save badge animates upwards while fading out

Key

	<i>very promising</i>
	<i>promising</i>
	<i>neutral</i>
	<i>concerns</i>
	<i>major concerns</i>
	<i>unrated</i>



By stacking the resulting ratings, a crude histogram could be constructed that allowed users to see at a glance what the community thought of a hypothesis. A co-worker dubbed it a "histographic." It proved to be richer than stars or likes because it showed a distribution of votes in a compact space. The black dot indicates the computer's best guess.

Welcome Ramon Felciano [logout](#)

INGENUITY SYSTEMS Search [Advanced...](#)

Home | Leaderboard | Hypotheses | Watchlist |

Search Results

Filter: pathogen: Ebola end point: cell migration drug: ING:u2b [clear all](#)

Sort by: # pathogens | Display - 10 | From: 12/28/2004 | To: Today | Showing Unprioritized

1-10 of 23,456 results

- Inhibiting SERPINE1 would counteract Ebola pathogenesis**
serpin, peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor... species: **homo sapiens** type: **other** 2 pathogens 78 genes
- Inhibiting ITGAM would counteract Ebola pathogenesis**
alpha M (complement component 3 receptor 3 subunit) species: **mus** type: **other** 2 pathogens 78 genes
- Activating INS1 would counteract Ebola pathogenesis**
Insulin 1 species: **rattus** type: **other** 2 pathogens 67 genes
- Inhibiting TFGB1 would counteract Ebola pathogenesis**
transforming growth factor, beta 1 species: **rattus** type: **growth factor** 1 pathogen 36 genes
- Inhibiting RAC1 would counteract Ebola pathogenesis**
serpin, peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor... species: **mus** type: **other** 1 pathogen 75 genes
- Activating RAC1 would counteract Ebola pathogenesis**
ras-related C3 butulinum toxin substrate 1 (rho family, small GTP... species: **mus** type: **enzyme** 1 pathogen 74 genes
- Inhibiting CDH1 would counteract Ebola pathogenesis**
cadherin 1, type1, E-cadherin (epithelial) species: **mus** type: **enzyme** 1 pathogen 29 genes
- Inhibiting STAT3 would counteract Ebola pathogenesis**
integrin, alpha M (complement component 3 receptor 3 subunit) species: **mus** type: **transcription regulator** 1 pathogen 55 genes

My Ratings

- very promising (12)
- promising (34)
- neutral (4)
- concerns (23)
- major concerns (14)
- Unrated (4,756)

Virus (4657)

- Ebola (999)
- Marburg (1234)
- Lassa (1234)

Bacteria (2045)

- B.Anthraxis (1237)
- F.Tularensis (1047)
- Y.Pestis (963)

Intervention

- [activate \(5050\)](#)
- [inhibit \(3000\)](#)

Affected Pathogens

1 or more

Disease

- [hemorrhagic fever](#)
- [influenza](#)
- [colon cancer](#)
- [more](#)

Cellular Location

- [Antigen presenting cells](#)
- [astrocytes](#)
- [AT2 Cells](#)
- [B lymphocytes](#)
- [B Lymphocytes](#)
- [basophils](#)
- [more](#)

A high-def wireframe of a user browsing search results with filters applied. The resulting prototype tested extremely well. Instead of asking questions about the interface, users became engrossed and started conducting actual research.

Welcome Ramon Felciano [logout](#)

INGENUITY SYSTEMS Search [Advanced...](#)

Home | Leaderboard | Hypotheses | Watchlist |

HYPOTHESIS REPORT

Inhibiting ITGAM would counteract Ebola pathogenesis ratings (9) score 4

Target	ITGAM
Description	integrin, alpha M (complement component 3 receptor 3 subunit)
Type	other
Intervention	Inhibition
Pathogens	Ebola
Endpoints	cell death
Sub-cellular Loc.	Plasma membrane
Existing Drugs	
Expression in Cells	J774, RAW 264.7, THP-1
Genes (78)	CD4, CD 28, CHUK, CHUK-Ikbb-Ikbg, Ebola Virus, ...

Target Verification

In vitro	verified (TMT0445-6, Bavari 2010-06)
Ex vivo	Failed (TMT0610)
In vivo	--

Comments (2) and ratings (8) [History](#)

You Wed May 26, 2011 **Private**
Lorem ipsum dolor sit amet, consectetur adipiscing elit. Donec sodales rutrum orci, vitae hendrerit ligula pellentesque eu. Curabitur id massa magna, sit amet gravida ipsum. Vivamus turpis urna, feugiat in rutrum id, malesuada sit amet metus. [edit](#)

Ed Michol Mon May 24, 2011
Lorem ipsum dolor sit amet, consectetur adipiscing elit. Donec sodales rutrum orci, vitae hendrerit ligula pellentesque eu. Curabitur id massa magna, sit amet gravida ipsum. Vivamus turpis urna, feugiat in rutrum id, malesuada sit amet metus.

Justine Kent Mon May 24, 2011
Justine Kent has not entered a review workflow - rating, commenting, becoming a champion, taking a champion, if I am a champion, I can create a report

Subject Experts

- you
- [Justine Kent](#)
- [Ed Michol](#)
- [Gary Sanders](#)

Watched by:

- you
- [Albert Jenkins](#)
- [Jane Jones](#)
- [Justine Kent](#)
- [Ed Michol](#)

Prioritized at milestone

milestone:	Exercise 2
date:	11/03/09
contact:	Ed Michol

enlarge

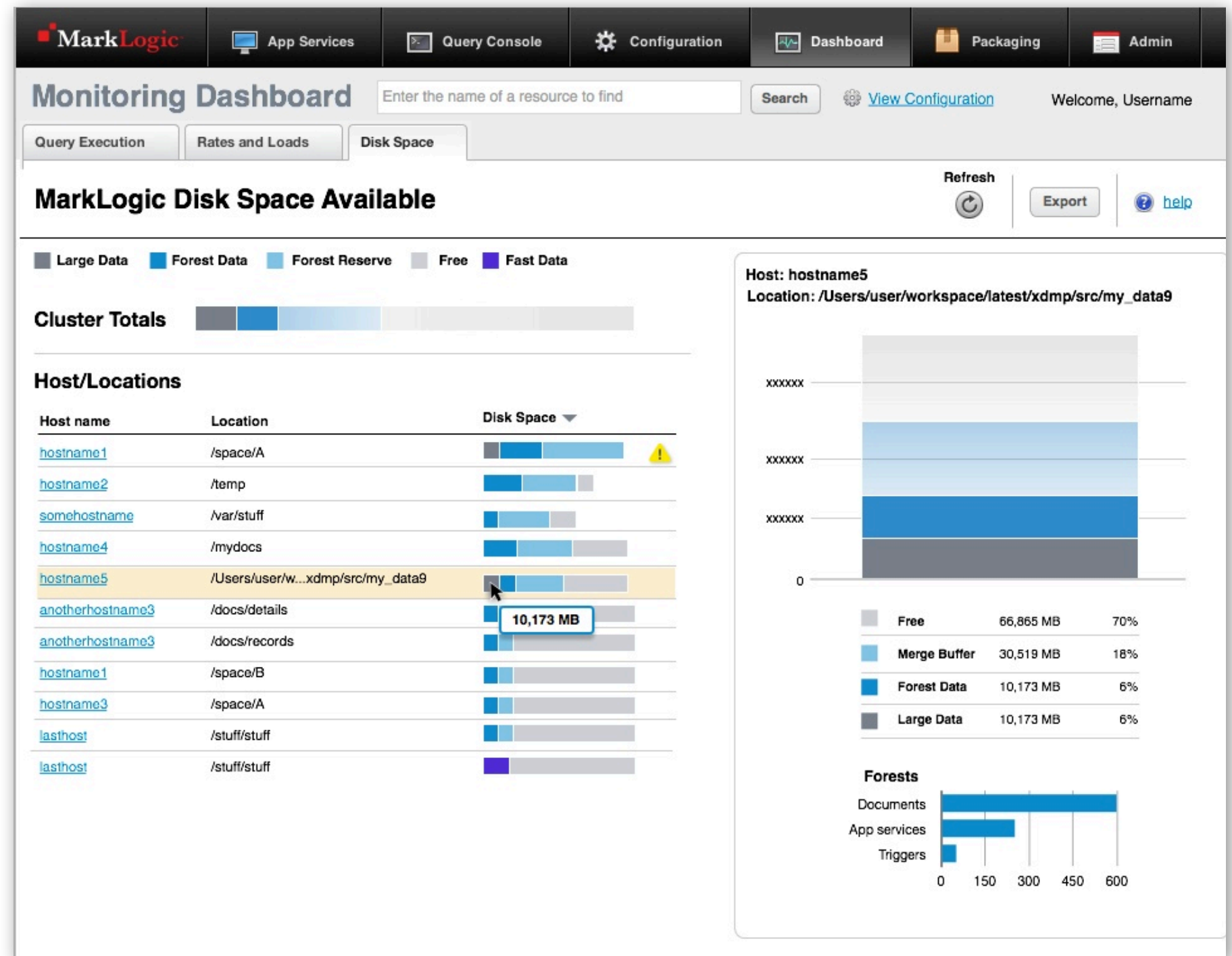
A high-def wireframe of a hypothesis detail page.

MarkLogic tools

While at MarkLogic, I also worked on server tools for the MarkLogic product, a few examples of the finished screens are included here. I conducted a number of site visits and interviews to better understand the needs of the users and issues they faced when developing MarkLogic applications.

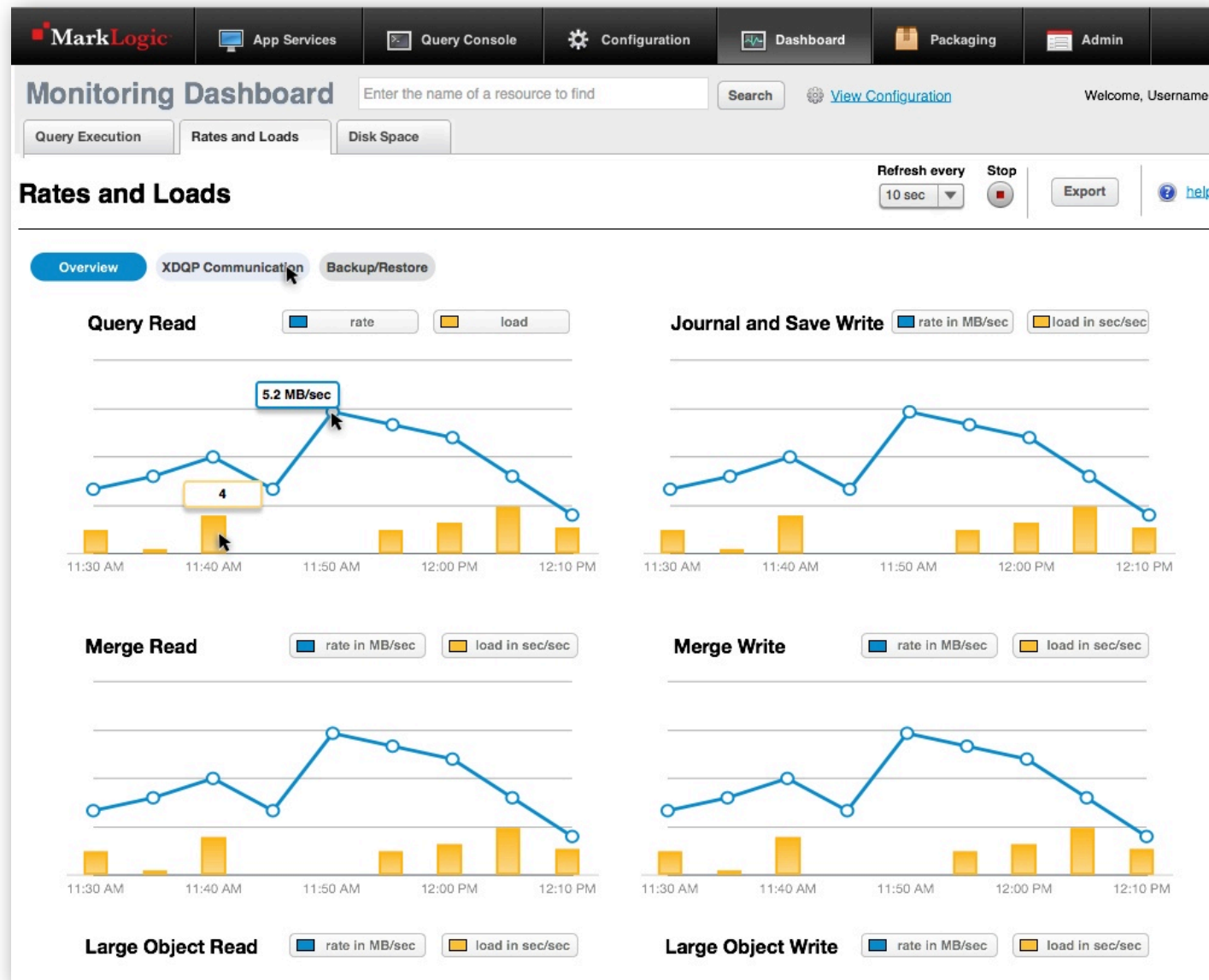
Contribution

- Facilitating product ideation
- Product and user research
- Storyboarding
- Wireframing
- Visual design
- HTML/CSS
- Usability testing



The MarkLogic disk dashboard

MarkLogic



A screenshot of the Rates and Loads monitoring interface. Through research we found that it was important for users to see differences between disk and CPU usage and chose a line over bar chart.

```
<pre>001 <results>
002   {
003     for $b in doc("http://bstore1.example.com/bib.xml")/bib/book,
004       $t in $b/title,
005       $a in $b/author
006     return
007       <result>
008         { $t }
009         { $a }
010       </result>
011   }
012 </results>
```

Module:Line No.	Count	Shallow %	Shallow µs	Deep %	Deep µs	Expression
.main:18:8	8	22	816	23	856	fn:contains(fn:string(\$par), \$spartner/text())
.main:3:39	1	15	564	16	603	fn:doc("company-data.xml")/descendant::company[nar
.main:20:4	3	10	381	11	410	<news_item>{ \$item/title } { \$item/date }</news_item>
.main:16:4	6	9	340	14	517	fn:contains(fn:string(\$par), "Foobar Corporation")
.main:9:32	1	7.4	281	76	2858	fn:doc("string.xml")/descendant::news_item
.main:11:2	3	5.3	201	57	2167	some \$t in \$item/descendant::title satisfies fn:contains(\$t/text(), \$spartner/text()) or (some \$par in \$item/descendant::par satisfies fn:contains(fn:string(\$par), \$spartner/text()))
.main:16:13	6	4.7	177	4.7	177	fn:string(\$par)
.main:17:10	5	4.3	162	31	1164	some \$spartner in \$foobar_partners satisfies fn:contains
.main:18:17	5	3.9	146	3.9	146	fn:string(\$par)
.main:15:6	3	2.8	104	48	1827	some \$par in \$item/descendant::par satisfies fn:contains(\$par/text(), \$spartner/text())
.main:7:0	1	2.3	87	97	3681	let \$foobar_partners := local:partners/"Foobar Corporate \$t in \$item/descendant::title satisfies fn:contains(\$t/text(), "Foobar

A screenshot of QueryConsole, an in-browser xquery IDE used it to query against the MarkLogic database.

thanks for looking

JD Vogt

Additional examples of my work, primarily web-based, can be found at:

www.jdvogt.com.

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